

Figure 1(a)

HHV8PEP	- - - - - MTPRSR-LATLGTVILLVCFCAG--AAHSRGDTFQ--
RHESRHADPEP	- - - - - MMITNRTRRLRAWVIIAIGTAVG--ENVTTPKGAT--
MURH68PEP	- - - - - MYPTVKSMRVAHLTNLLCCLCHTHLYVCQPTTLR--
BOVINEH4PEP	YYKTILFFALIKVCSFNQTTTHSTTSPLSISSTSSTTSKPSNTTNSSLAASPQ
ATELINEH3PEP	- - - - - MTLNR--CVLLIVLTFSTACS-----Q--
SAIMIRIPEP	- - - - - MVPNK--HLLLIIISFSTACG-----Q--
EQH2PEP	- - - - - MGVGGGPRVVLCLWCVAALLCQGVQAQEVVAETTPFA--
EQH5PEP	- - - - - MVAWFGLWGFARLMATLALLCGRVALDESSATPSIPP--
ALCELPEP	- - - - - MAHTGSTVCAFLIFAVLKNVFCQTPSSSEVEDVIPEAN-
EBVPEP	- - - - - MTRRRVLSVVVLLAALACRLGA----Q--TPEQ--
HHV8PEP	--TSSSPPTPGSSSKAPTPGEEASGPKSVDFYQFRVCAS-ITGELFRFNLEOTCPDTK
RHESRHADPEP	--TTAKPTP-GPS--TPTPP---ENPPR-AEAFKFRVCAS-ATGELFRFNLEKTCPGTE
MURH68PEP	--QPSDMTP-AQDAPTEPPPLSTNTNR--GFEYFRVCVGA-ATGETFRFDLDKTCPSTQ
BOVINEH4PEP	NTSTSXPSTDNQGTSTPTIPTVTDDTAS-KNFYKYRVCSASSSSGELFRFDLDQTCPDTK
ATELINEH3PEP	--TTPASSDEN--GKTPAIKEK-EYF---K-YRVCSAS-TTGELFRFNLDRAACPSTE
SAIMIRIPEP	--TTPTTAVEK--NKTQAIYQ-EYF---K-YRVCSAS-TTGELFRFDLDRTCPSTE
EQH2PEP	--THRPEVVAEE--NPANP----FLP----F--RVC GAS PTGGEI FRF PLE E SCPNTE
EQH5PEP	--THKPAVHHED--NTTNP----FLL----F--RVC GAS PTG-EIFRF PLE E NC PNTE
ALCELPEP	--TVSDNIIRQQR--NNTAKGIIHSDPSA---FPFRVCAS-NIGDIFRFQTS HSCPNTK
EBVPEP	--PAPPATTVQP--TATRQ---QTS---FPFRVCELS-SHGDLFRFSSDIQCPSFG
HHV8PEP	DKY-HQEGLLVLVYKKNIVPHIFKVR RYRKIATSVTVYRGLTES--AITNKYELPRPVPLY
RHESRHADPEP	DKT-HQEGLMVFKKNIVPHIFKVR RYRKVATS VTVYR GWTET--AVTGKQE VIRPV PQY
MURH68PEP	DKK-HVEGLLVLKKNIVPYIFKVR RYRKIATSVTVYR GWSQA--AVTNRDDISRAIPYN
BOVINEH4PEP	DKV-HREGILLVYKKNIVPHIFKVR RYKKIATSVR IFNGWSREGVAITNKWELSRAVPKY
ATELINEH3PEP	DKV-HKEGILLVYKKNIVPYIFKVR RYKKITTSVRI FNGWTREGVAITNKWELSRAVPKY
SAIMIRIPEP	DKD-HIEGIALIYKTNIVPYVFMVR KVR KLTSTTIYKGWSED--AITNQHTRS YAVPLY
EQH2PEP	DKE-HVEGILLIYKTNIVPYIFMVR KVR KLTSTTIYKGWSQD--AITNQYTSSFAMPLW
EQH5PEP	DKE-HNEGILLIFKENIVPYVFKVR KVR KIVTTSTIYNGIYAD--AVTNQHVFSKSVPIY
ALCELPEP	TRENHTEG LLMVFKDNIIIPYSFKVRSYTKIVTNILYNGWYAD--SVTNRHEEKFSVDSY
EBVPEP	
HHV8PEP	EISHMDSTYQCFSSMKVN VNGVENTFTDRDVNTTVFLQPV EQLTDN I QRYFSQPVIAE
RHESRHADPEP	EINHMDTTYQCFSSMRVN VNGIVN TYTDRDFTNQTVFLQPV EQLTDN I QRYFSQPVLYTT
MURH68PEP	EVGDFDSIYQCYNSATMV VNNVRQVYDRDGVN KTVNIRPV DGLTGNI QRYFSQPTLYSE
BOVINEH4PEP	EISMIDRTYHCFSAMATVINGILNTYIDRDSENKS VPLQPVAGL TENIN RYFSQPLIYAE
ATELINEH3PEP	EINLMDK NYQCHNCM QIEVNGMLNSY YDRDGNNKTVDLKPV DGLTGAI TRYISQPKVFAD
SAIMIRIPEP	EIDIMDKT YQCHNCM QIEVNGMLNSY YDRDGNNKTVDLKPV DGLTGAI TRYISQPKVFAD
EQH2PEP	EVQMMMDHYYQCFSAVQVNEGGHVNTYYDRDGWNETAFLKPADGLTSSITRYQS QPEVYAT
EQH5PEP	EARLVDNYECYNGIQTENGHTTYVDRDGYNESVRLVPADGLTSSIRRYHSQPELYVT
ALCELPEP	ETRRMDT IYQCYNSLDTVVGNNLLVYTDNGSNMVTDLQPV DGLSNSVR RYHSQPEIHAE
EBVPEP	ETDQMDT IYQCYNAVKMTKDGLTRVYVDRGVNITVNLKPTGGLANGVRRYASQTELYDA
HHV8PEP	PGWFGPIYR VRTTVNCEIVDMIARS AEP NYFVTSLGDTVEVSPFCYNESSCST-TPSNK
RHESRHADPEP	PGWFGPIYR VRTTVNCEIVDMIARS AEP SYFVTALGDTVEVSPFC HNDSTCSV-AEKTE
MURH68PEP	PGWMPGFIYR VRTTVNCEIVDMVARSMDP NYIAT ALGDSLELSPF QT FDNTSQS-TAPKR
BOVINEH4PEP	PGWFGPIYR VRTTVNCEIVDMYARS VE PYTHFITALGDTIEISPFC HNSQCTTGNSTSR
ATELINEH3PEP	AGWLWGTYKTRTTVNCEIVEMFARSADPYTYFVTALGDTVEVSPFCDAENSCPN---AS
SAIMIRIPEP	PGWLWGTYR TRTTVNCEIVDMFARSADPYTYFVTALGDTVEVSPFC DV D N S C P N ---AT
EQH2PEP	PRNLLWSYTTTRTTVNCEIVTEM SARS MKPFEFFVTSVGD TIEMSPFLKENGTEPE--KILK
EQH5PEP	PRNLLWSYTTTRTTVNCEIVDMT ARSHKPFEYFVTASGDSIETSPFY-T-NASR-----R
ALCELPEP	PGWL LGGYR RRTTVNCEIVTETDARAVP PFRYFITNIGDTIEMSPFW SKAWN ETEFS--GE
EBVPEP	PGWLW T YR TRTTVNCLITDMMAKSNSPF DFFVTTGQT VEMSPFYDGKNKETF---HE

Figure 1 (b)

HHV8PEP RHESRHDPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	NGLSVQVVLNHTVVTS DRG TS PTP QNR IF VET GAY TLS WASE SKT TAV C PL ALW KTF PR NGL GAR VL N Y TMV DFAT R -- APT T ETR V FAD SGEY TV SW KAED PKS A V CAL TLW KTF PR ADM RV REV K NY KF VD Y NN RG TA PA G Q S RT FLE TPS AT Y SW K TAT R QT AT CDL VHW KTF PR DAT KV WIE ENH QT VD YERRG - HPT KDK R IFL K DEE YT ISW KAED RERA ICDF V I WKT F PR DV LSS QVD FN H T VD YGN RATS SQ Q HGK R IFA HT D Y SVS WE A INK TT SVCS M VFW KGF QR DV LSV QID LN H T VD YGN RATS SQ Q HGK R IFA HT D Y SVS WE A VN KS AS VCS M VFW KFS QQR RPH S IQL LKN Y AVT K YGV GLG QAD N ATR FFA I FG D YSL SW KATTEN SSY CDL L I WKG FS N VP -- V QV L YN S V T D YGV GLG S G E N V T R F F A T L N D F S I S W K A A T E N S S Y C P L V L W K G F P S PD R T L T V A K D Y R V D Y K F R G T Q P Q G H T R I F V D K E E Y T L S W A Q Q F R N I S Y C R W A H W K S F D N RADS FH VRT NY KIV D YD N R G T N P Q G E R R A F L D K G T Y T L S W K L E N R - T A Y C P L Q H W Q T F D S
HHV8PEP RHESRHDPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	S IQTT HEDSF HFVANE IT AT F TAP -- LTPVANFTDTYSCLTSINTTLNASKAKLASTH A I QTT H EASY HFV AND V TAT F TSP -- LSEVANFTGTYSCLDEV I QKTLNDTIKKLSDTH A I QTAHEH S YHFV ANEV TAT F NTP -- L T E VENFTST YSCVSDQINKTISEYI QKLNNSY A I QTIHNE S HFV ANEV T ASFL TS NQE ET LRG NTE I LNC MNST INET LEET VKKF NKSH A I QTEHD STYHFIA NE ITAGFSTS -- KETLASFSSE YSCLMSD IN STLTDKIGRVNNTH A I QTEHD LTYHFIA NE ITAGFSTV -- KEPLANFTSDY CLMTH INT LED KIA RVNNTH A I QTNHNSL HFIA ND ITAS F STP -- LEEEAN - FNETFKCIWNNTQEEI QKKLKEVEKTH A I QTKHEKS YHFIA D A V T AS F YTP -- LTDETSYFNTTYQC AWQDIEGEI QKRFDPVSKTH A I KTEHGKSLHFV AND ITAS F YTP -- NTQTREVLGKH VCLNN TIESELKSRLAKVN DTH T I A T E TGKSIHFV T D E G T S S F V T N -- TTVGIELPDAFKCIEEQVNKT MHEKYE A VQDRY
HHV8PEP RHESRHDPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	VP - NGTVQYFHTTGGLYLVQPM SAINLTHAQ - GDSGNPTSSPPPSASP ----- M VT - NGSAQYYKTEGGLFLLWQPLTPLS LVDEM RGLNG -- TTPAP -- P ----- A VA - SGK TQYF KTDG NLYLIWQPLHEP EIDID - EDSDPEPTPAP -- P ----- K IR - DGEVKYYKTNGGLFLI WQAMKPLNLSEHT -- N-YTIER -- N ----- N VP - NGTAQYF KTEGGMILVWQPLTAIEEAMIEATT VSP TPLS ----- T TP - NGTAEYYQTEGGMILVWQPLIAIEEAMLEATT VSP TPLS ----- T RP - NGTAKVYKTTGNLYIVWQPLIQIDLLDTHAKLYNLNTATASPTSTP ----- AR - NGSVQIYKTSGNLYVWWQPLVQLDLLAAHAKTINSTDNSTSPTTAPN ----- TT SP - NGTAQYLYTNGGLL V WQPLVQQKLLDAKGLLDAVKKQNTTT ----- T TKG QEAITY FITSGGLL AWLPLT P RSLATVKNLTEL TPTSSPPSPS PAP SAARGST
HHV8PEP RHESRHDPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	TTSASRRKRRSASTAAAGG -- GGSTDN ----- LSYTQLQFAYDKLRDG IN QVLEEL SRA TTSTVSRVRRS VNTNEQ -- ATDN ----- LAAPQLQFAYDKLRASINKVLEEL SRA STRRKREAADNGNSTSEVS -- KGSEN P ----- LITAQI QFAYDKLTTSVNNVLEEL SRA KTGNKS RQKRS VDTKTFQG -- AKG -- LSTAQVQYAYDHRLRTSMNHILEEL TKT AHLT SRTGRRKRDVSAG -- SENS ----- VLLAQI QYAYDKL RQS IN NVLEEL AIT SSRSKRAIRDS V SAG -- SENN ----- VFLSQI QYAYDKL RQS IN NVLEEL AIT - TTS PRRRRR DTSS VSGGG -- NNGDNSTKEESVAASQVQFAYDNL RKS IN RVLGELSRA TSTSSRKR RDGTNTATNN -- SSSNNSSMEENLAT S QVQFAYDQLRKS IN RVLEQLSRV TTTR SRRQR RSV SSG IDV -- YTAEST -- ILLTQI QFAYDTLRAQINNVLEEL SRA PAAVLRRRRR DAGNATT P V PPTA PGKSL GTL NN PATVQI QFAYDSL RQINRMLGDLARA
HHV8PEP RHESRHDPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	WC REQVRDNLMWY ELSKINPT SVM TAIYGRPVSAKFVGDAISVTECINV DQSSVNIHKSL WC REQVRDTYMWY ELSKINPT SVM TAIYGRPVSAKFVGDAISVTD CV A VDQASVSIHKSL WC REQVRDTLMWY ELSKVNPT SVM SAIYGRPVVAARYVGDAISVTD CIYVDQSSVNIHQSL WC REQKKDNLMWY ELSKINPV SVM SAIYGRPVAVKAMGDAFMSEC INV DQASVNIHKSM WC REQV RQTMWY EIAKINPT SVM TAIYGRPVSAKALGDVISVTECINV DQSSVSIHKSL WC REQV RQTMWY EIAKINPT SVM TAIYGRPVSRKA LGDVISVTECINV DQSSVSIHKSL WC REQYRASLMWY ELSKINPT SVM SAIYGRPVSAKLG D VVSVSDCISVDQKSVFVHKNM WC QNQYRASLMWY ELSKINPT SVM SAIYGRPVSAKLG D VVSVSDCISVDQKSVFVHKNM WC REQH RASLMWNE LSKINPT SVM SSIYGRPVSAKRI GDVISVSHCVV DQDSVSLHRSM WC LEQKRQNMLV RELT KINPT SVM SSIYGRPVSAKRI GDVISVSHCVV DQDSVSLHRSM WC LEQKRQNMLV RELT KINPT SVM SSIYGRPVSAKRI GDVISVSHCVV DQDSVSLHRSM

Figure 1(c)

HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	RTN---SKDVCYARPLVTFKFLNSSNLFTGQLGARNEIILTNNQVETCKDTCEHYFITRN RTS---TPGMCYSRPPVTFRFLNSTTLFKGQLGPRNEIILTNDQVEACKETCEHYFIASN RLQH---DKTTCYSRPRVTFKFINSTDPLTGQLGPRKEIILSNTNIETCKDESEHYFIVGE RTD---DPKVCYSRPLVTFKFVNSTATFRGQLGTRNEIILTNTHVETCRPTADHYFFVKN KTT---NNDCYCYSRPPVTFKFVNSSLSQLFKGQLGARNEIILSESILVENCHQNAEHTAKN KTE---NNDICYCYSRPPVTFKFVNSSLSQLFKGQLGARNEIILSESILVENCHQNAEHTAKN KVPG---KEDLCYTRPVVGFKFINGSELFAGQLGPRNEIVLSTSQVEVCQHSCEHYFQAGN RVPG---SKDLCYTRPVVGFKFINGSELFVGQLGARNEIILSTNLVEVCQHSCEHYFQGGN RVPGRDKTHECYSRPPVTFKFINDSHLYKGQLGVNNEIILTTTAVEICHENTEHYFQGGN RVPG---SETMCYCYSRPLVSFSFINDTKTYEGQLGTDNEIFLTKKMTEVCQATSQYYFQSGN
HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	<u>ETLVYKDYAYLRTINTTDISTLNNTFIALNLSFIQNI</u> D KIAELYSSAEKRLASSV <u>FDLET</u> <u>V</u> TYYYYKDYVFVKKINTSEISTLGT <u>F</u> IALNLSFIENIDFRVIELYSRAEKKLGSV <u>FDIET</u> <u>Y</u> IYYYYKNYI FE EKLNSSIATLDT <u>F</u> IALNLSFIENIDFKTVELYSSTERK <u>LD</u> ASSV <u>FDIES</u> <u>M</u> THYFKDYKFVKTMDTNNISTLDTFLTLNLT <u>F</u> IDNIDFKTVELYSSTERKMAS - ALD <u>LET</u> <u>E</u> TYHFKNYLH V E T LP <u>L</u> TNISTLDTFLALNLT <u>F</u> IE <u>N</u> IDFKAVELYSSGERKLAN - VF <u>LET</u> <u>E</u> TYHFKNYVH V E T LP <u>V</u> NNISTLDTFLALNLT <u>F</u> IE <u>N</u> IDFKAVELYSSGERKLAN - VF <u>LET</u> <u>Q</u> MYKYKDYYVSTLNLT <u>D</u> IP <u>L</u> HMTLNL S VENIDFKVIELYSKTEKRLSN - VF <u>DIET</u> <u>H</u> IYKYKNY E YVSTMNLT <u>D</u> V <u>P</u> TLHMTLNL S VEN <u>V</u> DFQVIQLYSQKEKKLSN - VF <u>DIET</u> <u>N</u> MYFYKNYRHVKTMP <u>V</u> GD <u>V</u> ATLDTFMVLNL T VENIDFQVIELYSREEKR <u>M</u> ST - AF <u>DIET</u> <u>E</u> IHVYNDYHFKTIEL <u>D</u> GIA <u>L</u> QTFISLN <u>T</u> SLIENIDFASLELYS <u>R</u> DEQRASN - VF <u>LEG</u>
HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	<u>M</u> FREYNYYTHRLLAGLREDLDNTIDMNKERFVRDLSEIADLGGIKTVVVNVASSVUTLCG <u>M</u> FREYNYYTQRLAGLREDLDNTIDLN <u>R</u> DR <u>L</u> ARDLSEIADLG <u>D</u> VGR <u>T</u> VVVNVASSVITLFG <u>M</u> FREYNYYT <u>T</u> SLAGIKK <u>D</u> LDNTIDYN <u>R</u> DR <u>L</u> V <u>Q</u> DLS <u>M</u> ADLG <u>D</u> IGRSVVVVSSVUTFFS <u>M</u> FREYNYYTQKL <u>A</u> SL <u>R</u> REDLDNTIDLN <u>R</u> DR <u>L</u> V <u>K</u> D <u>S</u> EM <u>M</u> ADLG <u>D</u> IKVVNT <u>F</u> SGIVTVFG <u>M</u> FREYNYYA <u>Q</u> SI <u>SL</u> RK <u>D</u> FD <u>N</u> S <u>Q</u> RNN <u>R</u> DI <u>I</u> QDF <u>S</u> E <u>I</u> LA <u>D</u> LG <u>S</u> IGK <u>V</u> IVNIASSAFSLFG <u>M</u> FREYNYYA <u>Q</u> SI <u>SL</u> RK <u>D</u> FD <u>N</u> S <u>Q</u> RNN <u>R</u> DI <u>I</u> QDF <u>S</u> E <u>I</u> LA <u>D</u> LG <u>S</u> IGK <u>V</u> IVNVASGA <u>F</u> SLFG <u>M</u> FREYNYYT <u>Q</u> NL <u>N</u> GL <u>R</u> K <u>D</u> DD <u>S</u> I <u>D</u> H <u>G</u> R <u>D</u> S <u>F</u> I <u>Q</u> T <u>L</u> G <u>D</u> IM <u>Q</u> D <u>L</u> G <u>T</u> IGKVVVVNVASGV <u>F</u> SLFG <u>M</u> FREYNYYT <u>Q</u> NL <u>K</u> GL <u>R</u> K <u>D</u> DD <u>S</u> I <u>D</u> H <u>G</u> R <u>D</u> S <u>F</u> I <u>Q</u> FL <u>G</u> DL <u>V</u> Q <u>D</u> L <u>V</u> P <u>G</u> D <u>V</u> IVNVASGV <u>F</u> SLFG <u>M</u> FREYNYYT <u>Q</u> RV <u>T</u> GL <u>R</u> RD <u>L</u> <u>T</u> <u>D</u> -LATNRQFVD <u>A</u> FG <u>S</u> L <u>M</u> DL <u>U</u> LG <u>V</u> V <u>G</u> KT <u>V</u> LN <u>A</u> V <u>S</u> V <u>A</u> T <u>L</u> F <u>S</u> <u>I</u> FR <u>E</u> YNF <u>Q</u> A <u>Q</u> NI <u>AG</u> LR <u>K</u> D <u>U</u> DN <u>A</u> V <u>S</u> NG <u>R</u> N <u>Q</u> FD <u>G</u> L <u>E</u> LM <u>D</u> SL <u>G</u> SV <u>G</u> Q <u>S</u> IT <u>N</u> LV <u>S</u> TV <u>GG</u> L <u>F</u>
HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	<u>S</u> LV <u>T</u> GF <u>I</u> NF <u>I</u> KH <u>P</u> L <u>G</u> GM <u>L</u> <u>M</u> <u>I</u> <u>I</u> <u>I</u> <u>I</u> <u>F</u> ML <u>S</u> RR <u>T</u> NT <u>I</u> Q <u>A</u> P <u>V</u> K <u>M</u> I <u>Y</u> P - DVDRRA <u>S</u> IV <u>S</u> GF <u>I</u> NF <u>I</u> K <u>S</u> P <u>F</u> G <u>G</u> ML <u>M</u> <u>I</u> <u>L</u> <u>V</u> V <u>A</u> V <u>V</u> L <u>I</u> V <u>F</u> AL <u>N</u> R <u>R</u> T <u>N</u> A <u>I</u> Q <u>A</u> P <u>I</u> R <u>M</u> I <u>Y</u> P - DIDKM <u>Q</u> <u>S</u> IV <u>T</u> GF <u>I</u> FK <u>F</u> FT <u>N</u> PL <u>G</u> GI <u>F</u> ILL <u>I</u> <u>I</u> <u>G</u> GI <u>I</u> <u>F</u> L <u>V</u> V <u>V</u> L <u>N</u> R <u>R</u> N <u>S</u> OF <u>H</u> API <u>K</u> ML <u>P</u> VEN <u>Y</u> AR <u>Q</u> A <u>S</u> IV <u>V</u> GG <u>F</u> V <u>S</u> FF <u>T</u> N <u>P</u> IG <u>G</u> VT <u>I</u> <u>I</u> <u>L</u> <u>L</u> <u>I</u> <u>V</u> V <u>V</u> F <u>V</u> V <u>F</u> IV <u>S</u> RR <u>T</u> NN <u>M</u> NE <u>A</u> PI <u>K</u> MI <u>Y</u> P - NID <u>K</u> AS <u>G</u> IV <u>T</u> GI <u>L</u> N <u>F</u> IK <u>N</u> PL <u>G</u> GM <u>L</u> <u>T</u> <u>F</u> LL <u>V</u> G <u>A</u> <u>I</u> <u>I</u> <u>L</u> <u>V</u> <u>I</u> <u>L</u> <u>V</u> <u>R</u> <u>R</u> <u>T</u> NN <u>M</u> SQ <u>A</u> PI <u>R</u> MI <u>Y</u> P - DIE <u>K</u> SR <u>G</u> IV <u>T</u> GI <u>L</u> N <u>F</u> IK <u>N</u> PL <u>G</u> GM <u>F</u> <u>T</u> <u>F</u> LL <u>L</u> <u>I</u> <u>G</u> AV <u>I</u> <u>I</u> <u>L</u> <u>V</u> <u>I</u> <u>L</u> <u>V</u> <u>R</u> <u>R</u> <u>T</u> NN <u>M</u> SQ <u>A</u> PI <u>R</u> MI <u>Y</u> P - DVE <u>K</u> SK <u>S</u> IV <u>S</u> GV <u>I</u> FF <u>K</u> N <u>P</u> FG <u>G</u> ML <u>L</u> <u>I</u> <u>V</u> <u>L</u> <u>L</u> <u>I</u> <u>A</u> GV <u>V</u> V <u>V</u> Y <u>L</u> <u>F</u> M <u>T</u> R <u>S</u> R <u>S</u> I <u>Y</u> S <u>A</u> PI <u>R</u> ML <u>P</u> - GVERAA <u>S</u> IV <u>S</u> GV <u>I</u> FF <u>K</u> N <u>P</u> FG <u>G</u> ML <u>L</u> <u>F</u> GL <u>I</u> <u>A</u> AV <u>V</u> V <u>I</u> <u>T</u> V <u>I</u> <u>L</u> <u>N</u> R <u>K</u> A <u>K</u> R <u>F</u> A <u>Q</u> N <u>P</u> V <u>Q</u> M <u>I</u> <u>Y</u> P - DIKTIT <u>S</u> IV <u>S</u> GV <u>I</u> FF <u>K</u> N <u>P</u> FG <u>G</u> ML <u>L</u> <u>I</u> <u>L</u> <u>V</u> <u>L</u> <u>V</u> <u>A</u> G <u>V</u> V <u>V</u> I <u>L</u> <u>V</u> <u>I</u> <u>S</u> TR <u>R</u> R <u>T</u> QM <u>S</u> QQ <u>P</u> V <u>Q</u> M <u>L</u> <u>P</u> - GIDE <u>L</u> A
HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	<u>P</u> -----SGGAP <u>T</u> REE <u>I</u> KN <u>I</u> LL <u>G</u> M <u>H</u> QL <u>Q</u> -----ERQ <u>K</u> ADD <u>L</u> KK <u>S</u> TP <u>V</u> Q <u>R</u> T <u>AN</u> GL <u>R</u> <u>P</u> -----SGGKV <u>D</u> QE <u>Q</u> I <u>K</u> NI <u>L</u> AG <u>M</u> H <u>Q</u> QL <u>Q</u> -----EERR <u>L</u> DE <u>Q</u> Q <u>R</u> S <u>A</u> PS <u>L</u> F <u>R</u> AS <u>D</u> GL <u>K</u> <u>PP</u> YSA---SPPA <u>I</u> D <u>K</u> E <u>E</u> I <u>K</u> R <u>I</u> LL <u>G</u> M <u>H</u> Q <u>V</u> H <u>Q</u> -----EEKE <u>A</u> Q <u>K</u> Q <u>L</u> T <u>N</u> SG <u>P</u> TL <u>W</u> Q <u>K</u> AT <u>G</u> FL <u>R</u> <u>E</u> QE-----NI <u>Q</u> PL <u>P</u> G <u>E</u> E <u>I</u> K <u>R</u> I <u>LL</u> G <u>H</u> Q <u>L</u> Q <u>Q</u> -----SEHG <u>K</u> SEE <u>E</u> ASH <u>K</u> P <u>G</u> FL <u>Q</u> LL <u>G</u> DL <u>Q</u> <u>S</u> -----SV <u>T</u> PT <u>E</u> PE <u>V</u> I <u>K</u> Q <u>I</u> LL <u>G</u> M <u>H</u> N <u>M</u> Q <u>Q</u> -----EEY <u>K</u> K <u>RE</u> E <u>H</u> K <u>A</u> Q <u>P</u> S <u>F</u> L <u>K</u> R <u>A</u> T <u>D</u> FL <u>S</u> <u>S</u> -----TV <u>T</u> PM <u>E</u> P <u>E</u> T <u>I</u> Q <u>I</u> LL <u>G</u> M <u>H</u> N <u>M</u> Q <u>Q</u> -----EAY <u>K</u> K <u>RE</u> E <u>Q</u> R <u>A</u> R <u>P</u> S <u>I</u> F <u>R</u> Q <u>A</u> E <u>E</u> FL <u>S</u> <u>Q</u> E-----GAHP <u>V</u> SE <u>D</u> Q <u>I</u> R <u>N</u> I <u>L</u> M <u>G</u> M <u>H</u> Q <u>F</u> Q <u>R</u> Q <u>R</u> A <u>E</u> E <u>A</u> R <u>R</u> EE <u>E</u> V <u>K</u> G <u>K</u> R <u>T</u> L <u>F</u> E <u>V</u> I <u>R</u> D <u>S</u> <u>QQ</u> -----NV <u>Q</u> PI <u>P</u> E <u>D</u> Q <u>V</u> R <u>S</u> I <u>L</u> AM <u>H</u> Q <u>F</u> Q <u>Q</u> Q <u>Q</u> Q <u>Q</u> Q <u>Q</u> Q <u>E</u> E <u>H</u> T <u>Q</u> -----RR <u>S</u> I <u>F</u> D <u>T</u> I <u>R</u> E <u>S</u> <u>S</u> Q <u>R</u> E <u>E</u> EL---Q <u>V</u> D <u>P</u> I <u>S</u> K <u>H</u> E <u>L</u> D <u>R</u> I <u>M</u> L <u>A</u> M <u>H</u> D <u>Y</u> H <u>A</u> S <u>K</u> -----Q <u>P</u> E <u>S</u> K <u>Q</u> D <u>E</u> E <u>Q</u> G <u>S</u> T <u>T</u> S <u>G</u> P <u>A</u> D <u>W</u> L <u>N</u> K <u>A</u> <u>QQ</u> H <u>A</u> S <u>G</u> E <u>G</u> P <u>G</u> I <u>N</u> P <u>I</u> S <u>K</u> T <u>E</u> L <u>Q</u> A <u>I</u> M <u>L</u> A <u>H</u> Q <u>N</u> -----EQ <u>K</u> R <u>AA</u> Q <u>R</u> A <u>A</u> G <u>P</u> S <u>V</u> A <u>R</u> L <u>Q</u> A <u>A</u> R

Figure 2

ATGGCAGGTA GCTTAAAAC TAGGGGATCT GTTCTAGCAC TGTGGTACCT GTATCAGGTG 60
GCTCTTTATT CACTTAGTAT AGCAGAGACC GGTGTAACCT CACCTCCAAA TACAGCGACC 120
TGGTCTACTG AATCGCCGCT AACAGGTACAC TATGGAACAC ACGATTCAAG CCATGGTGAA 180
AGAGGAAACAA ACGAAAACAG AGATTCAAGA GAGCAAATA AAAACATTTA TGATCGCCT 240
TCTACGTTTC CTTACAGAGT ATGCAGTGCC TCCGGAGTTG GAGATGTCTT TAGATTCAG 300
ACCGACCATG TGTGTCGGT GAAGCTGAT ATGGTACACA GTGAGGGGAT TCTACTAATT 360
TACAAACAGA ACATTATTCC ATTTATGTT AGAGTTAGGA AATATAGAAA AGTTGTTACA 420
ACAAGTACTG TCTACAATGG TATTTATTCT GACTCTATTA CCAACCAACA TACTTTCTAT 480
AAATCAATCG AACCTGGGA GACAGAAAAG ATGGACACAA TATATCAGTG TTTAATTCT 540
TTAAGACTAA ACACAGGTGG AAATCTGCTT ACTTATGTAG ATAGAGATGA TATAAATATG 600
ACAGTGTTC TGCAACCTGT TGACGGTGTG ACGCCCGATG TGAAGAGGTA TGGCAGTCAA 660
CCAGAGCTGT ACCTTGAACC TGGCTGGTT TGGGTAGTT ATAGAAGACG AACTACAGTG 720
AACTGTGAAC TAATGGACAT GTTTGAAGA TCAAATCCTC CATTGATTT CTTGTTACA 780
GCTACAGGTG ATACGGTGG AATGTCTCCA TTTTGGAGTG GTGAAGATGA TCATGAAAAT 840
AAGATGCAG AGAACCATG GTTTGTAGT GTGATAAATA ACTACAAGGT GGTGGACTAT 900
CAAACAGAG GGACTGTACC CCTTGGAAAA ACAAGGATAT TTCTAGATAG GGAAGAGTAT 960
ACATTATCTT GGGAAAAGCA TCTAAAAAAAT ATGTCATATT GTCCACTAAC ATTATGGAAA 1020
GCATTTTACA ATGGAATCCA GACGGAGCAT TCAGGCTCAT ATCATTGTTGT AGCCAATGAC 1080
ATCACAGCGT CATTCAACAC TAGTAAAGAA GACATGAAAG AGTTCAATAC GACATATCAT 1140
TGTCTCAACG AGGAAATAAA GGCAGAAATA GAGAAGAAAT ATGCAAAAGT AACTCAACT 1200
CACTCTAAAT ATGGAGATCT GAAATACTTT AAAACAGATG GGGGTCTCTA TTGAGTCTGG 1260
CAACCTCTTAA TTCAAAACAG GCTTCTTGAT GCTAAGAACAA AACTGAACAA TGAGACTTAT 1320
TCCAGGAGAT CACGACGTCA GGCAGAACATC ACTACTGACC CAATGATGGA GATGACTGGA 1380
AATGGGACAG GTGGAGAATA TAGCAGTGAA ATTCAATCA CGGTGGCGCA GGTGCAGTAT 1440
GCCTATGACA ATCTTCGTAT CAGAATAAT AACATTGGG AAGATTGTC AAAGGCATGG 1500
TGTGTTGAGC AGCATAGAGC TGCTCTGGTG TGGAAATGAGC TCAGCAAGAT TAATCCCACA 1560
ACCGTCATGA GCATGATTAA CAATAGACCC GTATCAGCCA AAAGAATAGG AGATGTCATT 1620
TCAGTCTCTA ACTGTATTGT GGTAGACCAA ACCAGTGTCT CATTACATAA AAGTCTCAGG 1680
CTTCTCAGTG CATCGGATGA AAAGTGTTC TCTAGACCTC CAGTGACATT TAAGTTTATG 1740
AATGACAGTA CTATTACAA AGGGCAACTA GGAGTCAATA ATGAGATTCT CTTAACACAA 1800
ACATACCTTG AAACATGTCA GGAAAACACT GAGTATTACT TTCAGGCAAA GACAGACATG 1860
TACATTTACA AAAACTATGA GCATTGAAAG ACTGTGCCTT TATCTTCGAT CACCACACTA 1920
GATACATTAA TAGCCCTTAA TTTTACACTA TTGGAGAATG TTGACTTTAA AGTCATTGAA 1980
CTTTATACCA GGGACGAGAA GAGGCTTAGT AATGTCCTTG ACATTGAAAC AATGTTTAGG 2040
GAATATAACT ACTATGCTCA GAGGGTCAGT GGCCTCAGAA AGGATTGCT GGATCTAAAGC 2100
ACCAATAGAA ATCAATTGT GGATGCATT GGTAGTCTTA TGGATGATTT GGGTGCTGTT 2160
GGGCAGACAG TTGTAATGC TGTAAGTGGT GTGGCTACGC TGTTTAGCTC AATTGTAACA 2220
GGATTTATTA ATTTCATTA AAACCCATTG GGTGGAATGT TAATGATTAT TGTTGTTATT 2280
GGTGTGCTAT TTGCCATCTA CTTTCTGACC AAAAAGACGA AGATATATGA GACGGCACCG 2340
ATTAAGATGA TTTATCCTGA AATTGACAAG CTGAAAGAAC GTGAGGGAAA ATCAGAAATA 2400
GCACCAATCA GTGAAGAAGA GCTGGAGAGA ATTGTACTTG CTATGCACAT CCATCAACAA 2460
AATTCAACATA TGGAAACAAA AACAAAGGAAG GATCCCAAAG ACAGCATATT AACAAAGGGCA 2520
CAAATATGC TACGAAAG ATCAGGATAT TCTAATTAA AAAATGCTGA ATCTGTGGAG 2580
ATGTTAAACA CTTTATAA 2598

Figure 3

MAGSLKLRGS VLALWLYQV ALYSLSLIAET GVTSPPTAT WSTESPLTGH	50
YGTHDSSHGE RGNNENRDSE EQNKNIYGP STFPYRVCSA SGVGDVFRFQ	100
TDHVCPDASD MVHSEGILLI YKQNIIPFMF RVRKYRKVVT TSTVYNGIYS	150
DSITNQHTFY KSIEPWETEK MDTIYQCFNS LRLNTGGNLL TYVDRDDINM	200
TVFLQPVDGV TPDVKRYGSQ PELYLEPGWF WGSYRRRTTV NCELMDFAR	250
SNPPFDFFVT ATGDTVEMSP FWSGEDDHEN KMHEKPWFVS VINNYKVVDY	300
QNRGTVPGLK TRIFLDREEV TLSWEKHLKN MSYCPLTLWK AFYNGIQTEH	350
SGSYHFVAND ITASFTTSKE DMKEFNTTYH CLNEEIKAEI EKKYAKVNST	400
HSKYGDLKYF KTDGGGLYLVW QPLIQNRLLD AKNKLNNETY SRRSRRQAES	450
TTDPMMEMTG NGAGGEYSSE NSITVAQVQY AYDNLRIRIN NILEDLSKAW	500
CREQHRAALV WNELSKINPT SVMSMIYNRP VSAKRIGDVI SVSNCIIVVDQ	550
TSVSLHKSLR LLSASDEKCF SRPPVTFKFM NDSTIYKGQL GVNNEILLTT	600
TYLETQCENT EYYFQAKTDM YIYKNYEHLK TVPLSSITTL DTFIALNFTL	650
LENVDFKVIE LYTRDEKRLS NVFDIETMFR EYNYYAQRVVS GLRKDLLDLS	700
TNRRNQFVDAF GSLMDDLGA VQTVVNAVSG VATLFSSIVT GFINFOKNPF	750
GGMMLIIIVVI GVLFAIYFLT KKTKIYETAP IKMIYPEIDK LKEREKGSEI	800
APISEEELER IVLAMHIHQO NSHMETKTRK DPKDSILTRA QNMLRKRSGY	850
SNLKNAESVE MLNTL	865

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Figure 4

pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	AATCT TCGTATCAGA ATAAATAACA CGCCGCCGTC CGGCTCCACG GTGGTGCAGC TGAGGCCGA GCAGGC--CT T G C GA A . C.	25 688
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	TTTTGGAAGA TTTGTCAAAG GCATGGTGTC GTGAGCACGA TAGAGCTGCT GCCCGAGTA CTCG-CAGGG GCGCAACTTC ACGGAGGGGA TCGCCGTGCT GA A T G CA G GC TC G G A T G TGCT	75 737
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	CTGGTGTGGA ATGAGCTAG CAAGATTAAT CCCACAAGCG TCATGAGCAT CT---T-CA AGGAGAACAT C-G-CC--C CGCACAAGT- TCAAGGCCA CT T A A GAG CA C G C CACAAG TCA G C	125 776
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	GATTTACAAT -AGACCCGTA TCAGC-CAAA AGAATAG-GA GATGTCATT CATCTACTAC AAGAACGTCA TCGTCACGAC CGTGTGGTCC GGGAGCACGT AT TAC A AGA C A TC C C A G T G G CA T	172 826
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	CAGTCTCTAA C-TGTATTG- -TGGTAGACC AAACCAGTGT CTCATTACAT ACGGGGCCAT CACCGAACCGC TTCACAGACC GCGTGGCCGT CCCCCTGCAG G C A C G A G T AGACC GT C C T CA	219 876
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	AAAAGTCTCA GGCTTCTCGAG TGCATCGGAT GAAAAGTGT TCTCTAGACC GAGA-TCACG GACGTGATCG ACCGCCG--C GGCAAGTGC GTCCTCA-AGG A A T C C C T G C CG G AAGTGC TCTC A A	269 922
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	TCCAGTGACA T--TTAA-GT TTATGA-ATG ACAGTACT-A TTTACAAAGG CCGAGT-ACG TGGCAACAA CCACAAGGTG ACCGCCTTCG ACCGGACGA C AGT AC T AA A A TG AC G T C AG	314 971
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	GCAACTAG-- GAGTCATAA TGAGATTCT- ---CTTAAC --CACAACA GAACCCCGTC GAGGTGGACC TGCGCCCCTC GCGCCTGAAC GCGCTCGCA G A C GAG TG G CT CT AAC C C	354 1021
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	TAC-C--TTG AAACA-TGTC -AGGAAA--- ACACTGAGTA TTAC-TTTCA CCCGGGCTG GCACACCACC AACGACACCT ACACCAAGAT CGGGCGCCG C C TG ACA C A GA A ACAC AG C C	395 1071
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	GGCAAAGACA GACATGTACA TTTACAAAAA CT--AT--- GAGCATTG GGCTTCTAC- CACACGGCA CCTCCGTCAA CTGATCGTC GAGGAGGTGG GGC AC ACA G CA T C AA CT AT GAG A TG	439 1120
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	AGAC-----TGTGCCTT TA-----TCT TCGATCACCA CACTAGATAC AGGCGCGCTC CGTGTACCCC TACGACTCCT TCGCCCTGTC CACGGGGAC AG C TGT CC TA CT TCG C CAC G AC	476 1170
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	ATT---TATA GCCCTTAATT TTAC--ACTA TTGGAGAATG TTGACTTTAA ATTGTGTACA TGCCCCCTT CTACGGCTG CGCGAGGGG CCCACGGGG ATT TA A C TT TAC T GAG G AC A	521 1220
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	AGTCATTGAA CTTTATACCA GGG----ACG AG-AAGAGGC TTAGTA--AT GCACATCG-G CTACCGGCC GGGCGCTTC AGCAGGTGGA GCACTACTAC CAT G CT CC GGG C AG G GG A TA A	564 1269
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	GTCTTGACA TTGAAACAAT G----- 585 CCCATCGAC- CTGGACTCGC GCCTCCGCC CT 1300 C T GAC TG A G	

Figure 5

pGHV-gpB prot PGHV1Prot. (491-850)	-----N LRI----- PAAPAAARRA RRSPGPAGTP EPPAVNGTGH LRITTGSAEF ARLQFTYDHI LRI	4 540
pGHV-gpB prot PGHV1Prot. (491-850)	--RINNILED LSKAWCREQH RAALVWNELS KINPTSVMSM IYNRPVSAKR QAHVNDMLGR IAAACELQN KDRTLWSEMS RLNPNSAVATA ALGQRVSARM N L AWC Q W E S NP V VSA	52 590
pGHV-gpB prot PGHV1Prot. (491-850)	IGDVISVSNC IVVDQTSVSL HKSLRLLSAS DEKCFSRPPV TFKFMNDSTI LGDVMAISRC VEV-RGGVYV QNSMR-VPGE RGTCYSRPLV TFE-HNGTGV GDV S C V V S R C SRP V TF N	102 637
pGHV-gpB prot PGHV1Prot. (491-850)	YKGQLGVNNE ILLTTTYLET CQENTEYYFQ AKTDMYIYKN YEHLKTVPLS IEGQLGDDNE LLISRDLIEP CTGNHRRYFK LGSGYVYYED YNYVRMVEVP GQLG NE L E C N YF Y Y V	152 687
pGHV-gpB prot PGHV1Prot. (491-850)	SITTLDTFIA LNFTLLENVD FKVIELYTRD E-----KR----- --ETISTRVT LNLTLLLEDRE FLPLEVYTR E LADTGLLDY SEIQRRNQLH T LN TLLE F E YTR E R	185 735
pGHV-gpB prot PGHV1Prot. (491-850)	----- ALKFYDIDRV VKVDHNVVLL RGIANFFQGL GDVGAAVGKV VLGATGAVIS	185 785
pGHV-gpB prot PGHV1Prot. (491-850)	-----LS NVF----- AVGGMVSFLS NPFGALAIGL LVLAGLVAAF LAYRHISRLR RNPMKALYPV LS N F	190 835
pGHV-gpB prot PGHV1Prot. (491-850)	-----DI E--TM----- TTKTLKEDGV DEGDV	195 850

Figure 6

pGHV-gpB DNA.txt pGHV2 DNA.txt	----- CCAGCATAAT GATAGCCAAT AATCTGTGTT ACTCTACCCT GATCTTAAAT	50
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- GACGAGGACG TGACGGGGAT CGACGAGAAA GATATTCTGA CGGTGCATGT AT T	5 100
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- TCGTATCAGA ATA-AAT-AA CATTGGAA GATTTGCAA AGGCATGGTG --AAACAAGA ATACCGTGTGTA CAGGTCG-T TAGGAG-CAG CGTCAGGGAG A AGA ATA T A CA TT G A G CA G CA GG G	53 146
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- TC-GTGAGCA GCATAGAGCT GCTCTGGTGT GGAATGAGCT CAGCAAGATT TCTATACTCG GCAC---GCT GCT---GTCT AG-ATG-GCT CAGGAAGAGA TC T C GCA GCT GCT GT T G ATG GCT CAG AAGA	102 188
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- AATCCCACAA GCG-TCATGA GCATGATTTA CAAT-AGACC CGTAT-CAGC AA---GGAA GTGAAGGCAGC GCATGAAACG CTGTGAGGAC CCTATGTTGG AA AA G G G GCATGA C T AG C C TAT T	149 234
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- CAAAGAATA GGAGATGTCA TTTCAGTCTC TAACTGTATT GTGGTAGACC C-ACTG-AT- -ACTTGACA -AGCAGCAGC TTGC--CCTC AAGGT-GAC- C A G AT A TG CA CAG C T C T GGT GAC	199 274
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- AAACCACTGT CTCATTACAT AAAAGTCTCA GGCTTCTCAG TGCATCGGAT -GTGCAATGC GTT-TTAC-- ---GGCTCA CGGGAGCC-G TGCA-CGG-T CA TG T TTAC G TCA G C G TGCA CGG T	249 314
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- GAAAAGTGCT TCTCTAGACC TCCAGTGACA TTTAAGTTTA TGAATGACAG CTGCTGC-CG TGTCT--CCC TCTAGCGCG TCCA---TCA CCAGC-ATAG G C T TCT CC TC AG G C T A T A A A AG	299 357
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- TACTATTAC AAAGGGCAAC TAGGAGTCAA TAATGAGATT CTCTAACCA GGC--GGGAC A---TGC--T TAGG---CA- -GACGAG-TG ACTTTATCAA C AC A GC TAGG CA A GAG T TTA C A	349 394
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- CAACATACCT TGAAACATGT CAGGAAACCA CTGAGTATTAA CTTTCAGGCC CAATGT-CCT T-----TCGT CTAGAGAATA CG----- CAA T CCT T GT C GA AA A C	399 420
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- AAGACAGACA TGTACATTAA CAAAAACTAT GAGCATTGAA AGACTGTGCC	449 420
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- TTTATCTTCG ATCACCAACAC TAGATACATT TATAGCCCTT AATTTACAC	499 420
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- TATTGGAGAA TGTGACTTT AAAGTCATTG AACTTTATAC CAGGGACGAG	549 420
pGHV-gpB DNA.txt pGHV2 DNA.txt	----- AAGAGGCTTA GTAATGTCTT TGACATTGAA ACAATG	585 420

Figure 7

pGHV-gpB prot	NLRIRINNIL EDLSKAWCRE QHRAALVWN E LSKINPTSV M SMIYNRPVSA	50
pGHV2 prot.txt	S--IMIANNL -----C---YSTLI--- LNDEDVTG----- IDE	25
	I I N L C S M L L T	
pGHV-gpB prot	KRIGDVISVS NCIVVDQTSV SLHKSRLLS ASDEKCFSRP PVTFKFMNDS	100
pGHV2 prot.txt	K---DILTVH ---VNKNNTV----- YRFVRSS	45
	K D V V V F S	
pGHV-gpB prot	---TIYKGQL GV-NNBILLT TTYLESTCQEN TEYYFQAKTD MYI---YKN-	142
pGHV2 prot.txt	VRESILGTLL SRWLRKRKEV KARMKRCEDP MLALILDKQO LALKVTCNAF	95
	I L C K	
pGHV-gpB prot	YEHLKTVP-- LSSITTLDTF IALNFITLL-E NVDFKVIELY TRD---EK-R	185
pGHV2 prot.txt	YGFTGAHVGL LPCLPLAASI TSIGRDMLRQ TSDFINNVLS SREYVSEKFS	145
	Y V L L DF L R EK	
pGHV-gpB prot	LSNV-F--DI ETM- 195	
pGHV2 prot.txt	LSDGDFQGDF SPEC 159	
	LS F D	

Figure 8

pGHV-gpB DNA AF118399 DNA.txt	AATCTTCGTA TCAGAATAAA TAACATTTG GAAGATTTGT CAAAGGCATG -----	50
pGHV-gpB DNA AF118399 DNA.txt	GTTGTCGTGAG CAGCATAGAG CTGCTCTGGT GTGGAATGAG CTCAGCAAGA -----	100
pGHV-gpB DNA AF118399 DNA.txt	TTAACATCCCAC AAGCGTCATG AGCATGATT ACAATAGACC CGTATCAGCC -----	150
pGHV-gpB DNA AF118399 DNA.txt	AAAAGAAATAG GAGATGTCA TTCAGTCTCT AACTGTATTG TGGTAGACCA -----	200
pGHV-gpB DNA AF118399 DNA.txt	AACCAGTGTC TCATTACATA AAAGTCTCAG GCTTCTCAGT GCATCGGATG -----	250
pGHV-gpB DNA AF118399 DNA.txt	AAAAGTGCTT CTCTAGACCT CCAGTGACAT TAAAGTTAT GAATGACAGT -----	300
	-----	14
	TAAT CTATGTCACT T AT ATG CA T	
pGHV-gpB DNA AF118399 DNA.txt	ACTATTTACA AAGGGCAACT AGGA-GTCAA TAATGAGATT CTCTTAACCA -CTACCC-TA ATCCATCATG AAGACCTGCA TAAATATCCT CAATTAAGG CTA A A A A GA T A TAA A T A TTAA	349 62
pGHV-gpB DNA AF118399 DNA.txt	CAACATACCT TGAAACATGT CAGGAAAACA CTGAGTATTA CTTTCAGGCA AGGAGGATTA TGAAACAT-----	399 83

	A TGAAACAT TTT TTT	
pGHV-gpB DNA AF118399 DNA.txt	AAGACAGACA TGTACATTTA CAAAAACTAT GAGCATTGAGA AGACTGTGCC -----	449 95
	TG ATT-----	

	AG TT CTG	
pGHV-gpB DNA AF118399 DNA.txt	TTTATCTTCG ATCACCAACAC TAGATACATT TATAGCCCTT AATTTACAC -----	499 99

	GTCC-----	
	GTCC	
pGHV-gpB DNA AF118399 DNA.txt	TATTGGAGAA TGTTGACTTT -----AAAG TCAT-T-GA A---CTT----- -----	534 139
	TGTT ACTTT AAA CAT T GA A CTT	
pGHV-gpB DNA AF118399 DNA.txt	-----TA----- TAC--CA-- G--GG--ACG AGA----- AG--AGG- TCTAACCTGC TTACAAACATG GCTGGCTAAG AGAAAAATGA TCAGAAAGGA TA TAC CA G GG A G AGA AG AGG	555 189
pGHV-gpB DNA AF118399 DNA.txt	CTTAGTA--A TGT-CT--TT GACA-TTGA- AACAATG----- ATTAGCAGCA TGTGCTGACC CAAAGCTCAG GACAAT-TTT AGATAAACAG TTAG A A TGT CT A A T A ACAAT	585 238
pGHV-gpB DNA AF118399 DNA.txt	-----	585
	CAGCTTGCAA TTAAGGTGAC ATGCAATGCT GTGTATGGGT TCACGGTGT	288
pGHV-gpB DNA AF118399 DNA.txt	-----	585
	TGCATCTGGT ATGCTGCCCT GTCTCAAGAT TGCAGAGACC ATAACATATGC	338
pGHV-gpB DNA AF118399 DNA.txt	-----	585
	AAGGAAGGGC CATGTTGGAA AAGACAAAAG TATTTGTAGA GAATTAAAGT	388
pGHV-gpB DNA AF118399 DNA.txt	-----	585
	CATGAGGATC TCCATTCCAT CTGTAAGGTT GGCTTTATGC CTCAGTCACC	438
pGHV-gpB DNA AF118399 DNA.txt	-----	585
	AAACAGCATT GATAAACCT TCAAGGTG	466

Figure 9

pGHV-gpB DNA AF118401 DNA.txt	GAGGACCTGC ATAAGTATCC TCAATTAAAG GAGGATGATT ATGAAACATT	50
pGHV-gpB DNA AF118401 DNA.txt	-----AATCTTC GTATCAGAAT TTTGATTAGT TCTGGCCCTG TTCACTTTGT AAAAAAACAC ATATCAGAAT AA C TATCAGAAT	17 100
pGHV-gpB DNA AF118401 DNA.txt	AAATAACATT TTGGAAGATT TGTCAAAGGC ATGGTGTGCGT GAGCAGCATA ----C-TC TT----- C T TT	67 105
pGHV-gpB DNA AF118401 DNA.txt	GAGCTGCTCT GGTGTGGAAT GAGCTCAGCA AGATTAATCC CACAAGCGTC ---CTG-TC- -----GAA- ---CTT--- -G-----CT CACAA---C CTG TC GAA CT G C CACAA C	117 125
pGHV-gpB DNA AF118401 DNA.txt	ATGAGCATGA TTTACAATAG ACCCGTATCA GCCAAAAGAA -----T-- ATG-GC-TG- -----GCCAAGAGAA AAATGATCAG ATG GC TG T	158 152
pGHV-gpB DNA AF118401 DNA.txt	--AGG-----AG-ATGT-----CA --TTT----- AAAGGAATTG ACAGCATGTG CTGATCCAA GCTCAGGACA ATTTTAGATA AGG AG ATGT CA TTT	172 202
pGHV-gpB DNA AF118401 DNA.txt	-----CAGTC T-----CTA--- ---AC-TGTA TTG-TG-GTA --GA-CCA-- AACAGCAGCT TGCAATTAAG GTGACATGCA ATGCTGTGTA TGGATTCACT CAG T TA AC TG A TG TG GTA GA CA	200 252
pGHV-gpB DNA AF118401 DNA.txt	-----A-----AC-CA G---TGTCTC A-----TTAC GGTGTGCAT CTGGTATGCT GCCATGTCTC AAGATTGCAG AGACCATCAC A A C G TGTCTC A TCAC	217 302
pGHV-gpB DNA AF118401 DNA.txt	-----AT AAAAGT--CT -CAG-GCTTC TATGCAAGGA AGGCCATGT TGGAAAAGAC AAAAGTATTT GTAGAGAATC A AAAAGT T AG G TC	235 352
pGHV-gpB DNA AF118401 DNA.txt	TCAG---TGC A---TCGGA T-GAAAAGT- -GCTT--CTC TAGACCTCCA TGAGTCATGA AGATCTCCGT TCCATATGTA AGGTTGGCTC TATACCTC-A T AG TG A TC G T A A GT G TT CTC TA ACCTC A	273 401
pGHV-gpB DNA AF118401 DNA.txt	GTGACATTAA GTTTATGAA TGACAGTACT ATTTACAAAG GGCAACTAGG GT--CA-TCA A---ACG-- TG----- TTT----- GT CA T A A A G TG TTT	323 417
pGHV-gpB DNA AF118401 DNA.txt	AGTCAATAAT GAGATTCTCT TAACCACAAAC ATACCTGAA ACATGTCAGG -G---ATAAA ----- G ATAA	373 423
pGHV-gpB DNA AF118401 DNA.txt	AAAACACTGA GTATTACTTT CAGGCAAAGA CAGACATGTA CATTACAAA -----	423 423
pGHV-gpB DNA AF118401 DNA.txt	AACTATGAGC ATTTGAAGAC TGTGCCTTTA TCTTCGATCA CCACACTAGA -----	473 423
pGHV-gpB DNA AF118401 DNA.txt	TACATTATA GCCCTTAATT TTACACTATT GGAGAATGTT GACTTTAAAG -----	523 423
pGHV-gpB DNA AF118401 DNA.txt	TCATTGAACT TTATACCAGG GACGAGAAGA GGCTTAGTAA TGTCTTGAC -----	573 423
pGHV-gpB DNA AF118401 DNA.txt	ATTGAAACAA TG 585 ----- 423	

Figure 10

Figure 11(a)

gi|2337975 (AF005370) glycoprotein B [Alcelaphine herpesvirus 1]
Length = 854

Score = 953 bits (2437), Expect = 0.0
Identities = 463/804 (57%), Positives = 589/804 (72%), Gaps = 26/804 (3%)

Query: 74 KNIYGSPSTFPYRVCASAGVGDVFRFQTDHVCPDASDMVHSEGILLIYKQNIIPFMFRVR 133
K I+ PS FP+RVCAS +GD+FRFQT H CP+ D H+EGILLI+K+NI+P++F+VR
Sbjct: 55 KGIHSFPSAFPPRVCASASNIGDIFRFQTSHPNTKDKHENEGILLIFKENIVPYVFKVR 114

Query: 134 KYRKVVTTSTVYNGIYSDSITNQHTFYKSIEPWETEKMDTIYQCFNSRLNNTGGNLLTYV 193
KYRK+VTTST+YNGIY+D++TNQH F KS+ +ET +MDTIYQC+NSL + GGNLL Y
Sbjct: 115 KYRKIVTTSTIYNGIYADAVTNQHVFSDKSVPIYETRRMDTIYQCYNSLDVTVGGNLLVYT 174

Query: 194 DRDDINMTVFLQPVDGVTPDVKRYGSQPELYLEPGFWGFSYRRRTTVNCELMDMFARSNP 253
D D NMTV LQPVDG++ V+RY SQPE++ EPGW G YRRRTTVNCE+ + AR+ P
Sbjct: 175 DNDGSNMTVDLQPVDGLSNVRRYHSQPEIHAEPGWLLGGYRRRTVNCEVTETDARAVP 234

Query: 254 PFDFEVATGDTVEMSPFWSGEDDHENKMHEKPWFVSVINNYKVVVDYQNRGTVPLGKTRI 313
PF +F+T GDT+EMSPFW + E + +V +Y+VVDY+ RGT P G TRI
Sbjct: 235 PFRYFITNIGDTIEMSPFWSKAWNTEFSGEPDRTLTVAKDYRVVDYKFRGTQPQGHTRI 294

Query: 314 FLDREETYLSWEKHLKNMSYCPLTLWKAFYNGIQTEHSGSYHFVANDITASFTTSKEDMK 373
F+D+EETYLSW + +N+SYC WK+F N I+TEH S HFVANDITASF T +
Sbjct: 295 FVDKEEYTLSWAQQFRNISYCRWAHWKSFDNAIKTEHGKSLHFVANDITASYTPNTQTR 354

Query: 374 EFNTTYHCLNXXXXXXXXXXXXXVNSTHSKYGDLKYFKTDGGLYLVWQPLIQNRLLDAKN 433
E + CLN VN THS G +Y+ T+GGL LVWQPL+Q +LLDAK
Sbjct: 355 EVLGKHVCLNNNTIESELKSRLAKVNDTHSPNGTAQYYLTNGGLLWWQPLVQQKLDAKG 414

Query: 434 KLN-----NETYSRRSRRQAESTTDPMMEMTGNGAGGEYSSSENSITVAQVQYAYDN 484
L+ T + RSRRQ S + +G Y++E++I + Q+Q+AYD
Sbjct: 415 LLDAVKKQQNTTTTTTRSRQRQRRSVS-----SGIDDVYTAESTILLTQIQFAYDT 466

Query: 485 LRIRINNILEDLSKAWCREQHRAALVWNELSKINPTSVMMSMIYNRPVSAKRIGDVISVS 544
LR +INN+LE+LS+AWCREQHRA+L+WNELSKINPTSVM S IY RPVSAKRIGDVISVS+
Sbjct: 467 LRAQINNVLEELSRAWCREQHRASLMWNELSKINPTSVMSSIYGRPVSAKRIGDVISVS 526

Query: 545 CIVVDQTSVSLHKSLLSA-SDEKCFSRPPVTFKFMDNSTIYKGQLGVNNEILLTTYL 603
C+VVDQ SVSLH+S+R+ +C+SRPPVTFKF+NDS +YKGQLGVNNEILLTTT +
Sbjct: 527 CVVVDQDSVSLHRSMRVPGRDKTHECYSRPPVTFKFINDSHLYKGQLGVNNEILLTTAV 586

Query: 604 ETCQENTEYYFQAKTDMYIYKNYEHLKTVPLSSITTLDTFIALNFTLLENVDFKVIELYT 663
E C ENTE+YFQ +MY YKNY H+KT+P+ + TLDTF+ LN TL+EN+DF+VIELYT+
Sbjct: 587 EICHENTEHYFQGGNNMYFYKNYRHVKTMPVGDVATLDTFMVLNLVENIDFQVIELYS 646

Query: 664 RDEKRLSNVFDIETMFREYNYYAQRVSGLRKDLLDLSTNRNQFVDAFGSLMDDLGAVGQT 723
R+EKR+S FDIETMFREYNYY QRV+GLR+DL DL+TNRNQFVDAFGSLMDDLG VG+T
Sbjct: 647 REEKRMSTAFDIETMFREYNYYTQRVTGLRRDLTDLATNRNQFVDAFGSLMDDLGAVGKT 706

Figure 11(b)

Query: 724 VVNAVSGVATLFSSIVTGFINFINKPFGGMLMIVVIGVLFAIYFLTKKTKIYETAPIKM 783
V+NAVS VATLFSSIV+G INFINKPFGGML+ ++ V+ + L +K K + P++M
Sbjct: 707 VLNAVSSVATLFSSIVSGIINFINKPFGGMLLFGLIAAVVITVILLNRKAKRFAQNPVQM 766

Query: 784 IYPEIDKLKEREKGKSEIAPISEEEELERIVLAMHIHQQNShMETK-----TRKDPKDSI 836
IYP+I + + + + PIS+ EL+RI+LAMH + + E+K T P D
Sbjct: 767 IYPDIKTITSQREELQVDPISKHELDRLIMLAMHDYHASKQPESKQDEEQGSTTSGPAD-W 825

Query: 837 LTRAQNMLRKRSGYNSNLKNAESVE 860
L +A+N+LR+R+GY LK +S E
Sbjct: 826 LNKAKNVLRRAGYKPLKRTDSFE 849